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FIGURE 1A

CACTGTGCGTATTGTGATGGCGCCTACGACCAGATCGGCTTCCCCAACCTCGAGCTCCAA
1-----+-----+-----+-----+-----+-----+-----+60
GTGACACGCATAACACTACCGCGGATGCTGGTCTAGCCGAAGGGTTGGAGCTCGAGGTT
H C A Y C D G A Y D Q I G F P N L E L Q
GTCCACAACCTCCTGGCTCTTCTTCCCTTGGCACCGCTTCTACCTCTACTTCCACGAGAGG
61-----+-----+-----+-----+-----+-----+-----+120
CAGGTGTTGAGGACCGAGAAAGGAACCGTGCGGAAGATGGAGATGAAGTGCTCTCC
V H N S W L F F P W H R F Y L Y F H E R
ATCCTCGGAAAGCTCATAGGCGACGACACTTTCGCCCTCCCTTCTTGGAACCTGGGACGCG
121-----+-----+-----+-----+-----+-----+-----+180
TAGGAGCCTTTCGAGTATCCGCTGCTGTGAAAGCGGGAGGAAAGACCTTGACCCCTGCGC
I L G K L I G D D T F A L P F W N W D A
CCCCGGCGCATGAAGCTGCCGTCGATCTACGCCGACCCCTTCGTCCTCGCTCTATGACAAG
181-----+-----+-----+-----+-----+-----+-----+240
GGCCCGCCGTACTTCGACGGCAGCTAGATGCGGCTGGGAAGCAGGAGCGAGATACTGTTC
P G G M K L P S I Y A D P S S S L Y D K
TTTCGCGACGCCAAGCACCGCCGCGAGTCCTCGTCGACCTCGACTACAACGGAACCGAC
241-----+-----+-----+-----+-----+-----+-----+300
AAAGCGCTCGGTTTCGTGGTCCGGGTCAGGAGCAGCTGGAGCTGATGTTGCCCTTGGCTG
F R D A K H Q P P V L V D L D Y N G T D

FIGURE 1B

```

301-----+-----+-----+-----+-----+-----+-----+360
      CCTAGTTTCACCGACGACAGCAGATCGATCAGAACCTCAAGATCATGTACCGCAGGTG
      GGATCAAAGTGGCTGCGTCTCGTCTAGCTAGTCTTGGAGTTCTAGTACATGGCCGTCAC
      P S F T D A E Q I D Q N L K I M Y R Q V

361-----+-----+-----+-----+-----+-----+-----+420
      ATCTCCAACGGCAAGACGCCGTTGCTCTTCTTAGGCTCGGCTTACCGTGCCGCGACAAC
      TAGAGGTTGCCGTTCTGCGGCAACGAGAAGAAATCCGAGCCGAAATGGCACGGCCGCTGTTG
      I S N G K T P L L F L G S A Y R A G D N

421-----+-----+-----+-----+-----+-----+-----+480
      CCAAAACCCCGCGGGGCTCGCTCGAGAACATACCACACGGCCCCCGTCCACGGGTGGACT
      GGTTTGGGCGCGCGCCGAGCGAGCTCTTGTATGGTGTGCCGGGCAGGTGCCCCACCTGA
      P N P G A G S L E N I P H G P V H G W T

481-----+-----+-----+-----+-----+-----+-----+540
      GCGACAGAAAGCCCAATCTCGAGGACATGGGCAACTTCTACTCCGCGGGGCGCGAC
      CCGCTGTCTTCGGTTGGGTTAGAGCTCCTGTACCCGTTGAAGATGAGGCGCCCGCGCTG
      G D R S Q P N L E D M G N F Y S A G R D

541-----+-----+-----+-----+-----+-----+-----+582
      CCTATCTTCTTCGCCCCACCATTCAAATGTCGATCGCATGTGG
      GGATAGAAGAGCGGGTGGTAAGTTTACAGCTAGCGTACACC
      P I F A H S N V D R M W

```

FIGURE 2A

```

1-----+-----+-----+-----+-----+-----+-----+-----+60
TTGCCGTTTGGAAATTGGACGCGCGCGCGCATGAAGCTGCCGTCGATCTACGCCGAC
AACGGCAAAACCTTAACCCCTGCGCGCGCGCGTACTTCGACGGCAGCTAGATGCGGCTG
  L P F W N W D A P G G M K L P S I Y A D
61-----+-----+-----+-----+-----+-----+-----+-----+120
CCTTCGTCCTCGCTCTATGACAAAGTTTCGCGACGCCAAGCACCGCGCGTCTCTCGTC
GGAAGCAGGAGCGAGATACTGTTCAAAGCGCTGCGGTTTCGTGTCGGCGCCAGGAGCAG
  P S S S L Y D K F R D A K H Q P P V L V
121-----+-----+-----+-----+-----+-----+-----+-----+180
GACCTCGACTACAACGGAACCGACCCCTAGTTTCACCGACGCAGAGCAGATCGATCAGAAC
CTGAGCTGATGTTGCCTTGGCTGGGATCAAAGTGGCTGCGTCTCGTCTAGCTAGTCTTG
  D L D Y N G T D P S F T D A E Q I D Q N
181-----+-----+-----+-----+-----+-----+-----+-----+240
CTCAAGATCATGTACCGGCAGGTGATCTCCAACGGCAAGACGCCGTTGCTCTTCTTAGGC
GAGTTCTAGTACATGCCCGTCCACTAGAGTTGCCGTTCTGCGGCAACGAGAAGAAATCCG
  L K I M Y R Q V I S N G K T P L L F L G
241-----+-----+-----+-----+-----+-----+-----+-----+300
TCGGCTTACCGTGCCCGGCGACAACCCAAACCCCGCGGGCTCGCTCGAGAACATACCA
AGCCGAATGCACGGCCGCTGTTGGGTTTGGGGCCCGCCCGAGCGAGCTCTTGATGGT
  S A Y R A G D N P N P G A G S L E N I P

```

FIGURE 2B

CACGGCCCCGTCCACGGGTGGACTGGCGACAGAAAGCCAAACCAATCTCGAGGACATGGGC
301-----+-----+-----+-----+-----+-----+-----+360

GTGCCGGGCGAGGTGCCCCACCTGACCGCTGTCTTCGGTTGGGTTAGAGCTCCTGTACCCG
H G P V H G W T G D R S Q P N L E D M G

AAC TTCTACTCCGGGGCGCGACCCATATCTTCTCGCCCAACCATTCAAATGTCGATAGC
361-----+-----+-----+-----+-----+-----+-----+420

TTGAAGATGAGGCGCCCCCGCTGGGATAGAAAGCGGGTGGTAAGTTTACAGCTATCG
N F Y S A G R D P I F F A H S N V D S

ATGTGG

421----- 426

TACACC

M W

FIGURE 3A

```

GTTGCTCTTCTTAGGCTCGGCTTACCGTGCCGGCGACAAACCCCGCGGGGCTC
1-----+-----+-----+-----+-----+-----+-----+60
CAACGAGAAGAAATCCGAGCCGAATGGACGGCCGCTGTTGGTTTGGGGCCGCGCCGAG
  L L F L G S A Y R A G D N P N P G A G S

GCTCGAGAACATACCACACGGCCCCGTCACGGGTGGACTGGCGACAGAAACCAACCCAA
61-----+-----+-----+-----+-----+-----+-----+120
CGAGCTCTTGTAATGTCGGGGCAGGTGCCACCTGACCGCTGTCTTTGGTTGGTT
  L E N I P H G P V H G W T G D R N Q P N

TCTCGAGGACATGGGCAACTTCTACTCCGGGGCGGACCCCTATCTTCTCGCCCCACCA
121-----+-----+-----+-----+-----+-----+-----+180
AGAGCTCCTGTACCCGTTGAAGATGAGCGGCCCGCGCTGGGATAGAAAGCGGGTGGT
  L E D M G N F Y S A G R D P I F F A H H

TTCAAACGTCGACCGCATGTGGTACTTGTGGAAGAAGCTCGGCGGGAAGCATCAGGACTT
181-----+-----+-----+-----+-----+-----+-----+240
AAGTTTGCAGCTGGCGTACACCATGAACACCTTCTTCGAGCCGCCCTTCGTAGTCCTGAA
  S N V D R M W Y L W K K L G G K H Q D F

TAACGATAAGGACTGGCTCAACACCACCTTCCTCTTCTACGACGAGAATGCTGACTAGT
241-----+-----+-----+-----+-----+-----+-----+300
ATTGCTATTCCTGACCGAGTTGTGGTGAAGGAGAAGATGCTGCTCTTACGACTGAATCA
  N D K D W L N T T F L F Y D E N A D L V

```

FIGURE 3B

```
TCGAGTCAACCTCAAGGACTGCTTGCAGCCGGAGTGGCTTCTGTTACGATTACCAAGACGT
301-----+-----+-----+-----+-----+-----+-----+360
AGCTCAGTGGGAGTTCCTGACGAACGTCGGCCTCACCGAAGCAATGCTAATGGTTCTTGCA
R V T L K D C L Q P E W L R Y D Y Q D V

CGAGATCCCGTGGCTGAAGACCCGGCCGACTCCCAAGCCTTGAAGCGCGAGAAACCGC
361-----+-----+-----+-----+-----+-----+-----+420
GCTCTAGGGCACCGACTTCTGGGCCGGCTGAGGGTTTCGGAACCTCCGCGTCTTTTGGCG
E I P W L K T R P T P K A L K A Q K T A

AGCGAAACACTGAAAGCTACAGACGACGCCGTTCCCGGTGACGCTGCAATCCGCGGT
421-----+-----+-----+-----+-----+-----+-----+480
TCGCTTTTGTGACTTTCGATGTCGTCTCTGCGGCAAGGCCACTGCGACGTTAGCGGCCA
A K T L K A T A E T P P F P V T L Q S A V

GAGCACGACGGTGAGGAGGCCCAAGGTATCGAGGAGCGGCCAAGGAGAAGGAAGGAAGA
481-----+-----+-----+-----+-----+-----+-----+540
CTCGTGCTGCCACTCCTCGGGTTCCATAGCTCCTCGCCGTTCCCTTCTCCTTCTTCTTCT
S T T V R R P P K V S R S G K E K E E E E

GGAGGTCCTCATCGTGAGGGGATCGAGTTCGACCGCGACTACTTCATAAAGTTCGACGT
541-----+-----+-----+-----+-----+-----+-----+600
CCTCCAGGAGTAGCACCTCCCCTAGCTCAAGCTGGCGCTGATGAAGTATTTCAAGCTGCA
E V L I V E G I E F D R D Y F I K F D V
```

FIGURE 3C

```

CTTCGTGAACGCCACCGAGGGTGAGGGCATCACGCCGGGGCCAGCGAGTTCGCGGGCAG
601-----+-----+-----+-----+-----+-----+-----+660
GAAGCACTTGCGGTGGCTCCCACTCCCGTAGTGCGGGCCCGGTCGCTCAAGCGCCCGTC
    F V N A T E G E G I T P G A S E F A G S

CTTCGTCAACGTCCCGCACAAAGCACACAGCACGAAGAAGAGAAAGCTGAAGACGAG
661-----+-----+-----+-----+-----+-----+-----+720
GAAGCAGTTGCAGGGCGGTGTTTCGTGTTTCGTGTCGTTCTTCTCCTTCTTCGACTTCTGCTC
    F V N V P H K H K H S K K E K K L K T R

GCTCTGCCTGGGGATCACTGACCTGCTCGAGGACATCGGGGGCGGAGGACGACGACGCGT
721-----+-----+-----+-----+-----+-----+-----+780
CGAGACGGACCCCTAGTAGCTGGACGAGCTCCTGTAGCCCCCGCCTCCTGTCTGTCTCGCA
    L C L G I T D L L E D I G A E D D S V

GCTCGTCACCATCGTCCCGAAAGCCGAAAGGCAAGGTGTCGGTCGCCGCCCTCCGCAT
781-----+-----+-----+-----+-----+-----+-----+840
CGAGCAGTGGTAGCAGGGCTTTTCGGCCTTTCCCGTTCCACAGCCAGCGGCCGGAGCGTA
    L V T I V P K A G K G K V S V A G L R I

CGATTTCCCAAATTGAAGTAATACTATATATTTCTACTACCTATCAAGGAAATAAAAGC
841-----+-----+-----+-----+-----+-----+-----+900
GCTAAAGGGTTTAACTTCACTTATGATATATAAAGATGATGGATAGTTCCTTTATTTTCG
    D F P N * S N T I Y F Y Y L S R K I K A

CGCACCATCGTAACAAAAA
901-----+-----+-----+-----+-----+-----+-----+925
GCGTGGTAGCATTTGTTTTTTT
    A P S * Q K K K

```

FIGURE 4A

```

GTTGCTCTTCTTAGGCTCGGCTTACCGTGCCGGTGACCAAGCCTAACCCCGCGCGGGATC
1-----+-----+-----+-----+-----+-----+-----+60
CAACGAGAAAGATCCGAGCCGAATGCCACGGCCACTGGTCGGATTGGGGCCGCGCCCTAG
  L L F L G S A Y R A G D Q P N P G A G S

CATCGAGAACATGCCGCACAAACGTCACCTTGTGGACCGGCGACCCAGCCACCCAA
61-----+-----+-----+-----+-----+-----+-----+120
GTAGCTCTTGTACGGCGTGTGTTGCACGTGAACACCTGGCCGCTGGCGTGGTCCGGTT
  I E N M P H N N V H L W T G D R T Q P N

CTTCGAGAACATGGGCACCTTCTACGGCGGCGCGCACCCCATCTTCTTCGCCACCA
121-----+-----+-----+-----+-----+-----+-----+180
GAAGCTCTTGTACCCGTGGAAGATGCCCGCGCGCGCTGGGGTAGAAGACGGGTGGT
  F E N M G T F Y A A A R D P I F F A H H

CGCCAACATCGACCCGAATGTGGTACCTGTGGAAGAAGCTCAGCAGGAAGCACCGACTT
181-----+-----+-----+-----+-----+-----+-----+240
GCGGTTGTAGCTGGCTTACACCATGGACACCTTCTTCGAGTCGTCCTTCGTGGTCCTGAA
  A N I D R M W Y L W K K L S R K H Q D F

CAATGACTCGGACTGGCTCAAAGCTTCCTTCCTCTTCTACGACGAGAACCGGACTTAGT
241-----+-----+-----+-----+-----+-----+-----+300
GTTACTGAGCCTGACCGAGTTTCGAAGGAAGGAGAAGATGCTGCTCTTGGCGCTGAATCA
  N D S D W L K A S F L F Y D E N A D L V

```


FIGURE 4B

```

TCGGGTACGGTCAAGGACTGCTTGAGACCGAGTGGCTGCGCTACACGTACCAAGACGT
301-----+-----+-----+-----+-----+-----+-----+360
AGCCCAGTGCCAGTTCTGTACGAACCTCTGGCTCACCGACGCGGATGTGCATGGTTCTGCA
R V T V K D C L E T E W L R Y T Y Q D V

GAAGATCCCATGGCGAACAACCCGACCGACTCCCAAGCTCGCAAGCGAGGAAAGCCGG
361-----+-----+-----+-----+-----+-----+-----+420
CTTCTAGGGTACCCGCTTGTGGGTGGCTGAGGGTTCGAGCGGTTCCGCTCCTTTCGGCC
K I P W A N T R P T P K L A K A R K A G

CAGCAGATCGCTGAAAGCCACCGGAGGTGCAGTTCCTGTGACGCTGGAATCCCCGGT
421-----+-----+-----+-----+-----+-----+-----+480
GTCGTCTAGCGACTTTCGGTGGCGCCTCCACGTCAAGGACACTGCGACCTTAGGGCCA
S R S L K A T A E V Q F P V T L E S P V

CAAAGTGACGGTGAAGAGGCCCAAGTGGGAGGAGCGGCAAGGAGAAGGAAATGAGGA
481-----+-----+-----+-----+-----+-----+-----+540
GTTTCACTGCCACTTCTCCGGGTTCACCCCTCCTCGCCGTTCTCCTTCTACTCCT
K V T V K R P K V G R S G K E K E D E E

GGAGATACTCATAGTGAGGGGATCGAGTTCGACCGGACTACTTCATCAAGTTCGACGT
541-----+-----+-----+-----+-----+-----+-----+600
CCTCTATGATATCACCTCCCTAGCTCAAGCTGGCGCTGATGAAGTAGTTCAAGCTGCA
E I L I V E G I E F D R D Y F I K F D V

```

FIGURE 4C

```

CTTCGTGAACGCGACGGAGGCGGACGGCATCACGGCCGGGCCAGTGAGTTCGCCGGCAG
601-----+-----+-----+-----+-----+-----+-----+660
GAAGCACTTGCGCTGCCCTCCCGCTGCCGTAGTCCCGGCCCGGTCACCTCAAGCGGCCGTC
    F V N A T E G D G I T A G A S E F A G S
CTTCGTGAACGTCCCGCACAGCACAGCACCGCAAGGATGAGAATAAGCTGAAGACGAG
661-----+-----+-----+-----+-----+-----+-----+720
GAAGCACTTGACAGGCGGTTCGTGTTTCGTGGCGTTCCTACTCTTATTCGACTTCTGCTC
    F V N V P H K H K H R K D E N K L K T R
GCTGTGCTGGGAATCACCGACCTGCTCGAGGACATCGGCGCGGAGACGACGACGCGT
721-----+-----+-----+-----+-----+-----+-----+780
CGACACAGACCCCTTAGTGGCTGGACGAGCTCCTGTAGCCGCGCCTCCTGCTGTGCTCGCA
    L C L G I T D L L E D I G A E D D S V
GCTCGTCACCATCGTGCCGGAAGGCAGGCAAGAAAGGTGTCCGTGCGCGGTCTTCGGAT
781-----+-----+-----+-----+-----+-----+-----+840
CGAGCAGTGGTAGCACGGCTTCCGTCCGTTTCCCTTTCCACAGGCAGCCGCCAGAACCTA
    L V T I V P K A G K G K V S V G G L R I
TGACTTTTCCAAGTGAGGAAATAAAAGAAATTCACGTGCCGTGCCCTGCTTCAATGTACGA
841-----+-----+-----+-----+-----+-----+-----+900
ACTGAAAAGGTTCACTCCTTTATTTCTTAAGTGACGGCACGGACGAAAGTTACATGCT
    D F S K * G N K R I H V P C L L S M Y E
ATAAAATAAGAGTGTCATCATCACCGACCATGGTTCTACTTTAAAAAAAATAAAAAAAA
901-----+-----+-----+-----+-----+-----+-----+960
TATTTTATCTCAGCTAGTAGTGGCTGGTACCAAGATGAAATTTTTTTTTTTTTTTT
    * N K S A S S P T M V L L * K K K K K

```

FIGURE 5A

```

1-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+60
GATCCGACGTTTGCGTTGCCATATTGGAACCTGGGATCATCCAAAGGCAATCGGTTTGCCA
CTAGGCTGCAAAACGCAACGGTATAACCTTGACCCTAGTAGGTTTCCCGTACGCAAAACGGT
D P T F A L P Y W N W D H P P K G M R L P

61-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+120
CACATGTTTGATCAACCAACGCTGTACCCCTGATCTTTACGATCCAAGACGTAAACCAAGAA
GTGTACAAACTAGTTGGTTTGACACATGGGACTAGAAATGCTAGGTTCTGCATTTGGTTCTT
H M F D Q P P N V Y P D L Y D P R R N Q E

121-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+180
CACCGCGGTTCTGTAATCATGGACCTTGGTCAATTTTGGTCAAGACGTGAAAGGAACTGAC
GTGCGCGCAAGACATTAGTACCTGGAACCAAGTAAACCAAGTTCTGCACCTTTCCTTGACTG
H R G S V I M D L G H F G Q D V K G T D

181-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+240
TTGCAAAATGATGAGCAATAACCTTACTCTAATGTATCGTCAAAATGATTACCAATTACCA
AACGTTTACTACTCGTTATTGGAATGAGATTACATAGCAGTTTACTAATGGTTAAGTGGT
L Q M M S N N L T L M Y R Q M I T N S P

241-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+300
TGTCACAACCTCTTTTTCGGTAAGCCATATTGTACGGAAGTTGGACCCAAACAGGCGAG
ACAGGTGTTGAGAAAAAGCCATTTCGGTATAACATGCCTTCAACCTGGGTTTGGTCCCGTC
C P Q L F F G K P Y C T E V G P K P G Q

```

FIGURE 5B

GGAGCTATTGAAAAACATCCCTCATACTCCTGTCCACATTTGGGTTGGTAGTAAGCCTAAT
301-----+-----+-----+-----+-----+-----+-----+360

CCTCGATAACTTTTGTAGGGAGTATGAGGACAGGTGTAACCCCAACCATCATTCGGATTA
G A I E N I P H T P V H I W V G S K P N

GAGAACTAACTGTAAAAACGGTGAAGATATGGGAAATTTCTATTTCAGCTGGTAAGGATCCT
361-----+-----+-----+-----+-----+-----+-----+420

CTCTTATTGACATTTTGGCCACTTCTATACCCCTTTAAAGATAAGTCGACCATTCCTAGGA
E N N C K N G E D M G N F Y S A G K D P

GCCTTCTATAGTCACCATGCAAAATGTAGATCGCATGTGGACAATATGGAAAAACATTAGGA
421-----+-----+-----+-----+-----+-----+-----+480

CGAAAGATATCAGTGGTACGTTTACATCTAGCGTACACCTGTTATACCTTTTGTAAATCCT
A F Y S H H A N V D R M W T I W K T L G

GGAAAAACGCAAGGACATCAACAAGCCAGATTATTTGAACACTGAGTCTTTTCTACGAC
481-----+-----+-----+-----+-----+-----+-----+540

CCTTTTGGGTTCCCTGTAGTTGTTTCGGTCTAATAAACTTGTGACTCAAGAAAAAGATGCTG
G K R K D I N K P D Y L N T E F F F Y D

GAAAA

541----- 545

CTTTT

E

FIGURE 6A

```

1-----+-----+-----+-----+-----+-----+-----+-----+60
TGCACTGTGCGTATTGCAACGGTGCTTACAAAATTGGTGGCAAAGAGTTACAAGTCCATT
ACGTGACACGCATAACGTTGCCACGAATGTTTAAACCACCGTTTCTCAATGTTCAGGTAA
  H C A Y C N G A Y K I G G K E L Q V H F

61-----+-----+-----+-----+-----+-----+-----+-----+120
TCTCGTGGCTTTTTCCTTTTTCATAGATGGTACTTGTACTTCTATGAAAGAATCTTGG
AGAGCACCGAAAAAAGGAAAAGTATCTACCATGAACATGAAGATACTTCTTAGAACC
  S W L F F P F H R W Y L Y F Y E R I L G

121-----+-----+-----+-----+-----+-----+-----+-----+180
GCTCTTAAATGATCCTACTTTTGGTTTGCCATATTGGAACCTGGACCATCCAAAGG
CGAGAAATTAATTACTAGGATGAAACCAACGGTATAACCTTGACCCCTGGTAGGTTCC
  S L I N D P T F G L P Y W N W D H P K G

181-----+-----+-----+-----+-----+-----+-----+-----+240
GCATGCGTATACCTCCCATGTTTCGATCGTGAAGGTCTTCCCTTTACGACGAAAAACGTA
CGTACGCATATGGAGGGTACAAGCTAGCACTTCCCAGAAAGGAAATGCTGCTTTTTCAT
  M R I P P M F D R E G S S L Y D E K R N

241-----+-----+-----+-----+-----+-----+-----+-----+300
ACCAAAGTCACCGTAATGGAACCATAATTGATCTTGGTCATTTCCGGTCAAGAAGTCCAAA
TGTTTTCAGTGGCATTACCTTGGTATTAACTAGAACCAAGTAAAGCCAGTTCTTCAGGTTT
  Q S H R N G T I I D L G H F G Q E V Q T

```

FIGURE 6B

```
CAACTCAACTGCAGCAGATGACTAATAACTTAATAATGTATCGTCAAAATGATAACTA
301-----+-----+-----+-----+-----+-----+-----+360
GTTGAGTTGACGTCGTCCTACTGATTATTGAATTGATATTACATAGCAGTTTACTATTGAT
    T Q L Q Q M T N N L T I M Y R Q M I T N
ATGCTCCTTGCCCCCTTGCTCTTCTTTGGTCAGCCTTACCCTCTAGGAACATGATCCCAGTC
361-----+-----+-----+-----+-----+-----+-----+420
TACGAGGAACGGGGAACGAGAAGAAACCAGTCGGAATGGGAGATCCTTGACTAGGGTCAG
    A P C P L L F F G Q P Y P L G T D P S P
CAGGGATGGGCACCTATTGAAAACATCCCTCATACTCCTGTCCACATTTGGTTGGTAGTA
421-----+-----+-----+-----+-----+-----+-----+480
GTCCCTACCCGTGATAACTTTTGTAGGGAGTATGAGGACAGGTGTAAACCCCAACCATCAT
    G M G T I E N I P H T P V H I W V G S R
GGCTTGATGAGAATAATACGAAACACGGTGAGGATATGGGTAATTTTACTCGGCCGGTT
481-----+-----+-----+-----+-----+-----+-----+540
CCGAAC TACTCTTATTATGCTTTGTGCCACTCCTATACCCATTA AAAAATGAGCCGGCCAA
    L D E N N T K H G E D M G N F Y S A G L
TAGACCCGCTTTTCTATTCCCATCACGCCCAATGTGGACCCGGATGTGGTCCGAGTGGAAG
541-----+-----+-----+-----+-----+-----+-----+600
ATCTGGCGGAAAAGATAAGGGTAGTGCGGTTACACCTGGCCTACACGAGCTCACCTTTC
    D P L F Y S H H A N V D R M W S E W K A
```

FIGURE 6C

```

CCTTAGGAGGAAAGGATCTCACGCACAAAGATTGGTTGAACTCCGAGTTCCTTT
601-----+-----+-----+-----+-----+-----+660
GGAATCCTCCCTTTTCTCCCTAGAGTGCCTGTTTCTAACCAACTTGAGGCTCAAGAAA
    L G G K R R D L T H K D W L N S E F F F
TCTACGATGAAAA
661-----+----- 673
AGATGCTACTTTT
    Y D E

```

FIGURE 7A

```

1  TGCATTGTGCGTATTGCAACGATGCTTACACAATGGGTGACCAAAAAGTTACAAGTTCACC
   +-----+-----+-----+-----+-----+-----+-----+-----+
61  ACGTAACACGCATAACGTTGCTACGAATGTGTACCCACTGGTTTCAATGTTCAAGTGG
   H C A Y C N D A Y T M G D Q K L Q V H Q
   +-----+-----+-----+-----+-----+-----+-----+-----+
   AATCGTGGCTTTTCTCCCGTTTCATAGATGGTACTTGTACTTCTACGAGAGAATCTTGG
61  +-----+-----+-----+-----+-----+-----+-----+-----+
   TTAGCACCGAAAGAAGGGCAAAGTATCTACCATGAACATGAAGATGCTCTCTTAGAACC
   S W L F F P F H R W Y L Y F Y E R I L G
   +-----+-----+-----+-----+-----+-----+-----+-----+
121  GCTCCCTCATCGATGATCCAACTTTTGTCTCTGCCATATTGGAACCTGGACCATCCAAGCG
   +-----+-----+-----+-----+-----+-----+-----+-----+
   CGAGGGAGTAGCTACTAGGTTGAAAACGAGACGGTATAACCTTGACCCCTGGTAGGTTGCG
   S L I D D P T F A L P Y W N W D H P S G
   +-----+-----+-----+-----+-----+-----+-----+-----+
181  GCATGCGTTTGCCCTGCTATGTTTCGATGTCGAAGGTTCTTCCCTCTACGATGCAAGACGTA
   +-----+-----+-----+-----+-----+-----+-----+-----+
   CGTACGCAAACGGACGATACAAGCTACAGCTTCCAAGAAGGGAGATGCTACGTTCTGCGAT
   M R L P A M F D V E G S S L Y D A R R N
   +-----+-----+-----+-----+-----+-----+-----+-----+
241  ATCCACATGTCCGTAATGGAACCATAATCGATCTTGGTTTTTTCGGTGATGAAGTCAAAA
   +-----+-----+-----+-----+-----+-----+-----+-----+
   TAGGTGTACAGGCATTACCTTGGTATTAGCTAGAACCAAAAAGCCACTACTTCAGTTTTT
   P H V R N G T I I D L G F F G D E V K T

```


FIGURE 7B

```
CTAATGAAATACAGATGATAACTAACTTAATTCTAATGTATCGTCAAAATGATAACTA
301-----+-----+-----+-----+-----+-----+-----+360
GATTACTTTATGTCTACTATTGATTGTTGAATTAAGATTACATAGCAGTTTACTATTGAT
N E I Q M I T N N L I L M Y R Q M I T N

ATGCTCCATGCCCGCTGTTGTTCTTCGGAGAGCCTTACAGATTCCGGATCTAAACCCAATC
361-----+-----+-----+-----+-----+-----+-----+420
TACGAGGTACGGGCGACAAACAAGAAGCCCTCTCGGAATGTCTAAGCCTAGATTTGGGTTAG
A P C P L L F F G E P Y R F G S K P N P

CGGGCAGGGAACCATTGAAAACATTCTCTATACTCCGGTTCACATTTGGACTGGTACTG
421-----+-----+-----+-----+-----+-----+-----+480
GCCCCGTCCCTTGGTAACTTTTGTAGGAGTATGAGGCCAAGTGTAACCTGACCATGAC
G Q G T I E N I P H T P V H I W T G T V

TGCGGTGTACGGATTGGGTAATTGTGTGCCATCATACGGTGAGGATATGGTAATTCT
481-----+-----+-----+-----+-----+-----+-----+540
ACGCCACATGCCATAAACCCATTAAACACACGGTAGTATGCCACTCCTATACCCATTAAAGA
R C T D L G N C V P S Y G E D M G N F Y

ACTCAGCTGGTTTAGACCCAGTTTTTTACAGCCACCACGCCCAATGTGGACCGCATGTGGA
541-----+-----+-----+-----+-----+-----+-----+600
TGAGTCGACCAAAATCTGGGTCAAAAATGTCTGGTGTGGGTACACCTGGCGTACACCT
S A G L D P V F Y S H H A N V D R M W N
```

FIGURE 7C

601-----+-----+-----+-----+-----+-----+660
ATGAATGGAAAGCACTAGGAGGGGAAAAGAGGATCTCACAGACAATGATTGGTTAAACT
TACTTACCTTTTCGTGATCCTCCCTTTTCTTCCCTAGAGTGCTGTACTAACCAATTGA
E W K A L G G K R R D L T D N D W L N S
CGGAGTTCCTTTTCTACGACGAAAA
661-----+-----+----- 685
GCCTCAAGAAAAAGATGCTGCTTTT
E F F F Y D E

FIGURE 8A

```

TGCATTGTGCGTACTGCGACGGCGCGTATGACCAAAATCGGCTTCCCCGATCTCGAGATCC
1-----+-----+-----+-----+-----+-----+-----+-----+60
ACGTAACACGCATGACGCTGCCGCGCATACTGGTTAGCCGAAGGGCTAGAGCTCTAGG
  H C A Y C D G A Y D Q I G F P D L E I Q

AGATCCACAACCTCGTGGCTCTTCTTCCCTTGGCACCGGTTCTACCTCTACTTCAACGAGC
61-----+-----+-----+-----+-----+-----+-----+-----+120
TCTAGGTGTTGAGCACCGAGAAAGAAAGAACCGTGGCCCAAGATGGAGATGAAGTTGCTCG
  I H N S W L F F P W H R F Y L Y F N E R

GCATACTCGGGAAACTTATCGGCGACGACACGTTGCGGCTGCCCTTCTGGAACCTGGGACG
121-----+-----+-----+-----+-----+-----+-----+-----+180
CGTATGAGCCCTTTGAATAGCCGCTGCTGTGCAAGCGCGACGGAAGACCTTGACCCCTGC
  I L G K L I G D D T F A L P F W N W D A

CGCCGGGGGCATGCAGTTCCCGTCTATCTACACGGACCCCTTCATCCTCGCTATATGACA
181-----+-----+-----+-----+-----+-----+-----+-----+240
GCGGCCCCCGTACGTCAAGGGCAGATAGATGTGCCCTGGGAAGTAGGAGCGATATACTGT
  P G G M Q F P S I Y T D P S S S L Y D K

AGCTGCGTGATGCGAAGCACCAAGCCGCCGACTTTGATTGACCTCGACTACAATGACCCG
241-----+-----+-----+-----+-----+-----+-----+-----+300
TCGACGCACTACGCTTCGTGGTCGGCGGCTGAAACTGAACTGAGAGCTGATGTACCGTGGC
  L R D A K H Q P P T L I D L D Y N G T D

```

FIGURE 8B

```

301-----+-----+-----+-----+-----+-----+-----+-----+360
      ATCCTACCTTCTCCCTGAAGAACAGATTAAACCACAACCTCGCCGTCATGTACCGACAGG
      TAGGATGGAAGAGGGGACTTCTTGTCTAATTGGTGTGGAGCGGCAGTACATGGCTGTCC
          P T F S P E E Q I N H N L A V M Y R Q V

      TGATATCCAGTGGAAAGACACACAGAGCTGTTTATGGGCTCAGCGTACCGCGCCGGTGACC
361-----+-----+-----+-----+-----+-----+-----+-----+420
      ACTATAGGTCACCTTTCTGTGGTCTCGACAAATACCCGAGTCGCATGGCGGCCCACTGG
          I S S G K T P E L F M G S A Y R A G D Q

      AGCCTGACCCCGCGCAGGTTCTGTAGAGCAGAAGCCGCACGGCCCCGGTGCAATGTGTGGA
421-----+-----+-----+-----+-----+-----+-----+-----+480
      TCGGACTGGGGCCCGTCCAAGACATCTCGTCTTCGGCGTGCCGGGCCACGTACACACCT
          P D P G A G S V E Q K P H G P V H V W T

      CAGGTGATCGCAACCAGCCCCAATCGCGAAGACATGGGCACGCTCTACTCGGCGGCGTGGG
481-----+-----+-----+-----+-----+-----+-----+-----+540
      GTCCACTAGCGTTGGTCGGGTTAGCGCTTCTGTACCCGTCGGAGATGAGCCGCCGCACCC
          G D R N Q P N R E D M G T L Y S A A W D

      ACCCCGTTTTTTTCGCACACCACGGCAACATCGACCGCATGTGGTACGTGTGAGGAACC
541-----+-----+-----+-----+-----+-----+-----+-----+600
      TGGGGCAAAAAGCGTGTGGTGGCCGTTGTAGCTGGCGGTACACCATGCACACCTCCTTGG
          P V F F A H H G N I D R M W Y V W R N L

```

FIGURE 8C

601-----+-----+-----+-----+-----+-----+660
TTGGGGCAAGCACCGAACTTCACCGACCCCGACTGGCTCAACGCGTCCCTTCCCTGTTCT
AACCGCCGTTTCGTGGCGTTGAAGTGGCTGGGGCTGACCGAGTTGCCGAGGACGACAAGA
G G K H R N F T D P D W L N A S F L F Y
ACGACGAAAA
661-----+ 670
TGCTGCTTTT
D E

FIGURE 9A

```
TTGCCGTTTGGAAATGGGACGCCGGGGGGCATGCAGATCCCGGCCATCTACGCCGAC
1-----+-----+-----+-----+-----+-----+-----+60
AACGGCAAAACCTTAACCCCTGCGCGGCCCCCGTACGTCTAGGGCCGGTAGATGCGGGCTG
L P F W N W D A P G G M Q I P A I Y A D

GCTTCGTCCCGCTCTACGACAAGCTGCGCAATGCGAAGCACCAAGCCGCCGACTTGGTC
61-----+-----+-----+-----+-----+-----+-----+120
CGAAGCAGGGCGGAGATGCTGTTTCGACGCCGTTACGCTTCGTGTCGGCGGCTGAAACCCAG
A S S P L Y D K L R N A K H Q P P T L V

GACCTCGACTACAACGGCACCGACCCGACCTTCACCCCTGAGCAGCAGATCGCCCAAC
121-----+-----+-----+-----+-----+-----+-----+180
CTGAGCTGATGTTGCCGTGGCTGGCTGGAAGTGGGACTCGTCGTCTAGCGGGTGTG
D L D Y N G T D P T F T P E Q Q I A H N

CTCACCATCATGTACCGACAGGTGATATCCGGCGGGGAAGACGCCGGAGTTGTTATGGGC
181-----+-----+-----+-----+-----+-----+-----+240
GAGTGGTAGTACATGGCTGTCCACTATAGGCCGCCCTTCTCGGGCCTCAACAAATACCCG
L T I M Y R Q V I S G G K T P E L F M G

GGCGGTACCGCGGGGACGCGCCAGACCCGGCGCAGGCACTCTAGAGCTCGTGCCG
241-----+-----+-----+-----+-----+-----+-----+300
CGCCGCATGGCGCGCCCGCTGCGCGGTCTGGGCCCGCGTCCGTGAGATCTCGAGCACGGC
A A Y R A G D A P D P G A G T L E L V P
```

FIGURE 9B

301-----+-----+-----+-----+-----+-----+-----+360
CACAAACACGATGATTTGTGGACCGGCGACCCCAACCAACCGAAGACATGGGC
GTGTTGTGCTACGTAAACACCTGGCCGCTGGGGTTGGTTGGTTGCTGCTTCTGTACCCG
H N T M H L W T G D P N Q P N D E D M G

361-----+-----+-----+-----+-----+-----+-----+420
ACGTTCTACGGGGCGGCGGACCCCATCTTCTCGCCCCACCGGCAACGTCGACCGC
TGCAAGATGCGCGCGCCCTGGGGTAGAAGACGGGTGGTGCCGTTGCAGCTGGCG
T F Y A A A R D P I F F A H H G N V D R

421-----+-----+-----+-----+-----+-----+-----+480
ATGTGTACGTGTGGCGGAAACTCGGGGCGACGCCGCGATTTCACCGACCCCGACTGG
TACACCATGCACACCGCCTTTGAGCCCCCGTGCGTGCGCTAAAGTGGCTGGGGCTGACC
M W Y V W R K L G G T H R D F T D P D W

481-----+-----+-----+-----+-----+-----+-----+540
CTCAACGGTCCTTCTTCTACGACGAGAACGCGCAGCTCGTCCGCGTCAAAGTAAAG
GAGTTGCGCAGGAAGAGAAGATGCTGCTCTTGCGCGTTCGAGCAGGCGCAGTTTCATTTC
L N A S F L F Y D E N A Q L V R V K V K

541-----+-----+-----+-----+-----+-----+-----+600
GACTGCTTGAGCGCGACGCGCTGCGGTACACGTACCAGGACGTCGACATCCCGTGATC
CTGACGAACTCGCGGCTGCGCGACGCCCATGTGCATGGTCCCTGCAGCTGTAGGGCACCTAG
D C L S A D A L R Y T Y Q D V D I P W I

FIGURE 9C

```

AGTGCGAAGCCGACGCCGGAAGAAACACCGGGGGCGCTGCGCCTTCCACGACAGAGGCT
601-----+-----+-----+-----+-----+-----+-----+660
TCACGCTTCGGCTGCGGCTTCTTTGTGGCCCCCGCGACGCGGAAGGTGCTGTCTCCGA
S A K P T P K K T P G G A A P S T T E A

ATATTCCGGTGGTGGATAAGCCGGTGAGCTCTACGGTGGCGAGGCCGAAGACGGG
661-----+-----+-----+-----+-----+-----+-----+720
TATAAGGCCACGACCTATTTCGGCCACTCGAGATGCCACCGCTCCGGCTTCTGCCCC
I F P V V L D K P V S S T V A R P K T G

AGGAGTACTGGGGAGGAGGAGGTGTTGGTGGAGGGAATCGAGCTGGACAAGGACGTG
721-----+-----+-----+-----+-----+-----+-----+780
TCCTCATGACCCCTCCTCCACAACCACCACCTCCCTTAGCTCGACCTGTTCCCTGCAC
R S T G E E V L V V E G I E L D K D V

GCCGTGAAGTTCGACGTGTATATAACGCGCCGACACAAGGGTGGGCGCGGAGGCG
781-----+-----+-----+-----+-----+-----+-----+840
CGGCACTTCAAGCTGCACATATATTTCGGCGGCTGTGCTTCCCCACCCCGCCTCCGC
A V K F D V Y I N A P D N E G V G P E A

AGCGAGTTCGAGGAGCTTCGTCCAGGTCCCGCACAAAGCAAGGGGAAGAGGAG
841-----+-----+-----+-----+-----+-----+-----+900
TCGCTCAAGCTCCCTCGAAGCAGGTCCACGGGCTGTTCGTGTTCTTCCCCTTCTCCTC
S E F A G S F V Q V P H K H K K G K K E

```


FIGURE 9D

901-----+-----+-----+-----+-----+-----+-----+-----+-----+960
AAGCGAGGATTAAACGACGCTCAGGCTCGGATAACGGACCTGCTCGAGGACATCGGC
TTCCGCTCCTAATTTGCTGCGAGTCCGAGCCCTATTGCCCTGGACGAGCTCCTGTAGCCG
K A R I K T T L R L G I T D L L E D I G
GCCGAGGACGACGAGCGTGCTCGTCACGCTCGTGCCGAGGATAGGCGAGGGTTGGTC
961-----+-----+-----+-----+-----+-----+-----+-----+-----+1020
CGGCTCCTGCTCTCGCACGAGCAGTGCGAGCACGGCTCCTATCCGCTCCCCAACCCAG
A E D D E S V L V T L V P R I G E G L V
AAGTTGGTGGGCTAAGGATCGATTCTCCAAGTGATCAGCAGCAATTAATACATG
1021-----+-----+-----+-----+-----+-----+-----+-----+-----+1080
TTCCAACCAACCCGATTCCCTAGCTAAGAGGTTCACTAGTCGTCGTTAATTGATATGTAC
K V G G L R I D F S K * S A A N * L Y M
AAAGTAAAAAAATTGCATTTACCTACCTACCTATAGAAGAGAATAAATGCGTATGTAATCTGC
1081-----+-----+-----+-----+-----+-----+-----+-----+-----+1140
TTTCATTTTAAACGTAAATGGATGGATATCTCTCTTATTACGCATACATTAGACG
K V K K I A F T Y L * K R I N A Y V I C
CCCATTTGTCACTTTAAATTTCTCGAGCGTGTTCTGAATGAGAGTTGCATGTCATGCGCGC
1141-----+-----+-----+-----+-----+-----+-----+-----+-----+1200
GGGTAAACAGTGAAAAATTAAAGAGCTCGCACAAAGACTTACTCTCAACGTACGTACGCGCG
P I C H F * F L E R V L N E S C M H A R

FIGURE 9E

```

AGCCATAATGCCCTGGTATAGTGTAGTAGTTTAGGCGTGGATACGTATAACGTACGTATGC
1201-----+-----+-----+-----+-----+-----+-----+1260
TCGGTATTACGGACCATATCACATCATCAAAATCCGCACCTATGCATATTGCATGCATACG
S H N A W Y S V V V * A W I R I T Y V C
ATGTATAAGGAATAATGATGAGTTTACTATGCAAAAAAAAAAAAAAAAAAAAA
1261-----+-----+-----+-----+-----+-----+-----+1319
TACATATTCCTTATTACTACTCAAAATGATACGTTTTTTTTTTTTTTTTTTTTTTT
M Y K E * * * V Y Y A K K K K K K K K K

```

FIGURE 10A

CGGTATCGATAAGCTTGATCCAGTCGCTGGTTAGGTGTTACTATGGCCACCCTCTC
1-----+-----+-----+-----+-----+-----+-----+60
GCCATAGCTATTTCGAACTAGGTCACGGACCAATAATCCACATAAGTGATACCGGTGGAGAG
G I D K L D P V P G L G V F T M A T L S
TAAACTAGCTTCCCAACCAATAACACCTCCACTCTCCCCGCTCCCTCCTTTGCATGCTCC
61-----+-----+-----+-----+-----+-----+-----+120
ATTGATCGAAGGTTGGTTATTGTGGAGGTGAGAGGGCGGAGGAGGAAACGTACGAGG
K L A S Q P I T P P L S P L P P L H A P
TTCTCTCACCAAAGCTTCACCACCACTTCTCTCTCCCCCTGTAGGGTCCCAACCACCC
121-----+-----+-----+-----+-----+-----+-----+180
AAGAGTGGTTTTCGAAGTGGTGGTGAAGGAGAGGGGACATCCCCAGGGTTTGGTGGG
S L T K S F T T T F L S P V G V P N H P
CGTCATAAGATCTCATGCAAAATCTAAGAGCAACAAGAGAAATGCCGACAAGCCTGCCGGC
181-----+-----+-----+-----+-----+-----+-----+240
GCAGTATTCTAGAGTACGTTTAGATTCTCTCGTTGTCTCTACGGCTGTTCCGACGCCCG
V I R S H A N L R S N K R M P T S L R A
CGCATCGCCCGCGACCTACTCTCTGGGCCCTCGCGGGGCTTTACGGTGCCACCCTG
241-----+-----+-----+-----+-----+-----+-----+300
GCGTAGCGGGCGGCTGGATGAGGACCCGGGAGCCGCCCGAAATGCCACGGTGTGACC
A S P A A T Y S W A L G G L Y G A T T G

FIGURE 10B

```

GCTCGGCCTCAACCGTCGAGGGCGCGCCCTATCCTGGCTCCCGACCTCTCAACTTG
301-----+-----+-----+-----+-----+-----+360
CGAGCCGGAGTTGGCAGCTCGCCGGCGGGGGATAGGACCGAGGGCTGGAGAGTTGAAC
    L G L N R R A A A A P I L A P D L S T C
TGGGCGGCCTGCCGACCTCCCTGCCCTCCGCCCGACCGACAGTTTGCTGCCCGCCATACCA
361-----+-----+-----+-----+-----+-----+420
ACCGGGCGGAGCGGTGGAGGACGGAGCGGGGCTGGCTGTCAAACGACGGCGGTATGGT
    G P P A D L P A S A R P T V C C P P Y Q
ATCCACCATCATCGACTTCAAGCTCCCCCGGATCTGCTCCGCTTCGCTCCGGCCTGC
421-----+-----+-----+-----+-----+-----+480
TAGGTGGTAGCTGAAGTTCGAGGGGGCGCTAGACGAGGCGAAGCGCAGCCGGACG
    S T I I D F K L P P R S A P L R V R P A
GGCCCACTTGTTGACGCCGACTACCTGGCCAAGTATAAGAAGCGGTCGAGCTCATGAG
481-----+-----+-----+-----+-----+-----+540
CCGGTGAACCAACTGCGGCTGATGGACCGGTTTCATATTCTCCGCCAGCTCGAGTACTC
    A H L V D A D Y L A K Y K K A V E L M R
GGCCCTGCCGGCGACGCCGCAACTTCGTACAGCAAGCGAAAGTGCACGTGCGTA
541-----+-----+-----+-----+-----+-----+600
CCGGACGGCGGCTGCTGGCGCGTGAAGCATGTCGTTTCGCTTTCACGTGACACGCAT
    A L P A D D P R N F V Q Q A K V H C A Y

```

FIGURE 10C

```

601-----+-----+-----+-----+-----+-----+-----+660
      TTGCGACGGCGGTATGACCAAAATCGGCTTCCCGATCTCGAGATCCAGATCCACAACCTC
      AACGCTGCCGCGCATACTGGTTTAGCCGAAGGGCTAGAGCTCTAGGTCTAGGTGTTGAG
      C D G A Y D Q I G F P D L E I Q I H N S

661-----+-----+-----+-----+-----+-----+720
      GTGGCTCTTCTTCCCTTGGCACCGGTTCTACCTCTACTCCAACGAGCGCATACTCGGAA
      CACCGAGAAAGAAAGAACCGTGGCCAAAGATGGAGATGAGGTGCTCGCGTATGAGCCCTT
      W L F F P W H R F Y L Y S N E R I L G K

721-----+-----+-----+-----+-----+-----+780
      ACTTATCGGCGACGACACGTTTCGGCTGCCCTTCTGTGAACTGGGACGCCGGGGGGCAT
      TGAATAGCCGCTGCTGTGCAAGCGCGACGGAAGACCTTGACCCCTGCGCGCCCCCGTA
      L I G D D T F A L P F W N W D A P G G M

781-----+-----+-----+-----+-----+-----+840
      GCAGTTCCCGTCTATCTACACAGACCCTTCATCCTCGCTATATGACAAGCTGCCGTGATGC
      CGTCAAGGGCAGATAGATGTGTCTGGGAAGTAGGAGCGGATATACTGTTTCGACGCACCTACG
      Q F P S I Y T D P S S S L Y D K L R D A

841-----+-----+-----+-----+-----+-----+900
      GAAGCACCAGCCGCCGACTTTGATTGACCTCGACTACAATGGCACCAGTCCCTACCTCTC
      CTTCTGCTCGGCGGCTGAAACTAACTGGAGCTGATGTTACCGTGGCTAGGATGGAAGAG
      K H Q P P T L I D L D Y N G T D P T F S

```

FIGURE 10D

CCCTGAAGAACAGATTAAACCACAACCTCGCCGTCATGTACCGACAGGTGATATCCAGTGG
901-----+-----+-----+-----+-----+-----+-----+960
GGGACTTCTTGTTCTAATTGGTGTGGAGCGGCAGTACATGGCTGTCCACTATAGGTCACC
P E E Q I N H N L A V M Y R Q V I S S G
AAAGACGCCAGAGCTGTTTATGGGCTCAGCGTACCGCGCCGGTGACCGCCTGACCCCCGG
961-----+-----+-----+-----+-----+-----+-----+1020
TTTCTCGGTCTCGACAAATACCCGAGTCGTCATGGCGCGGCCACTGGTCGGACTGGGGCC
K T P E L F M G S A Y R A G D Q P D P G
CGCAGGCTCTGTAGAGCAGAAGCCGCACGCGCCCGGTGCAATGTGTGACAGGTGATCGCAA
1021-----+-----+-----+-----+-----+-----+-----+1080
GCGTCCGAGACATCTCGTCTTTCGGCGTGCCGGGCCACGTACACACCTGTCCACTAGCGTT
A G S V E Q K P H G P V H V W T G D R N
CCAGCCCCAATCGCGAAGACATGGGCACGCTCTACTCGCGCGGTGGACCCCGTCTTCTT
1081-----+-----+-----+-----+-----+-----+-----+1140
GGTCGGGTTAGCGCTTCTGTACCCGTGCGAGATGAGCCCGCCGACCCCTGGGCGAGAAGAA
Q P N R E D M G T L Y S A A W D P V F F
CGCACACCACGGCAACATCGACCGCATGTGGTACGTGTGGAGGAACCTTGGCGGCAAGCA
1141-----+-----+-----+-----+-----+-----+-----+1200
GCGTGTGGTGCCGTTGTAGCTGGCGGTACACCATGCACACCTCCTTGGAAACCGCCGTTTCGT
A H H G N I D R M W Y V W R N L G G K H

FIGURE 10E

```

1201-----+-----+-----+-----+-----+-----+1260
      CCGCAACTTCACCGACCCCGACTGGCTCAACGCGCTCCTTCCTGTTCTATGATGAGAAATGC
      GCGGTTGAAGTGGCTGGGCTGACCGAGTTGCGCAGGAAGGACAAGATACTACTCTTACG
      R N F T D P D W L N A S F L F Y D E N A

1261-----+-----+-----+-----+-----+-----+1320
      GCAGCTCGTCCGTGTTAAAGTAAAGACTGCTTAGAGGCCGACGCAATGCGGTACACATA
      CGTCGAGCAGGCACAATTTTCATTCTGACGAATCTCCGGCTGCGTTACGCCATGTGTAT
      Q L V R V K V K D C L E A D A M R Y T Y

1321-----+-----+-----+-----+-----+-----+1380
      CCAGGATGTAGAGATCCCCTGGCTCAAAGCAAAGCCGACGCCAAAGAGCGCCCTACAGAA
      GGTCCACATCTAGGGCACCGAGTTTCGTTTCGGCTGCGGTTTCTCGCGGATGTCTT
      Q D V E I P W L K A K P T P K S A L Q K

1381-----+-----+-----+-----+-----+-----+1440
      GATAAAGAGCAAGGTATCGACGCTGAAGGCAACACCAAGGGGACGACGACTACCACAGC
      CTATTCTCGTTCATAGCTGCGACTTCCGTTGTGGTTCCCCCTGCTGCTGATGGTCTG
      I K S K V S T L K A T P R G T T T T A

1441-----+-----+-----+-----+-----+-----+1500
      AGAGACTACATTTCCGGTGTGTGGATAAGCCGGTGAGTGCAACAGTGGCTAGACCGAA
      TCCTCTGATGTAAAGGCCACCGACCTATTTCGGCCACTCACGTTGTCAACCGATCTGGCTT
      E T T F P V V L D K P V S A T V A R P K

```

FIGURE 10F

1501-----+-----+-----+-----+-----+-----+-----+-----+-----+1560
GCCCAGGAGGAGTGGGAAGGAGAAGGAAGAGGAGGAGGTGTTGGTGGAGGGAAT
CCGGTCCTCCTCACCCCTTCCTCTTCCTTCTCCTCCTCCACACCAACCACTCCCTTA
A R R S G K E K E E E E E E V L V V E G I
CGAGTTGGAGAAGGACGTGTTTCGTGAAGTTTGATGTGTATATAAACTCGCCGGAGCACGA
1561-----+-----+-----+-----+-----+-----+-----+-----+-----+1620
GCTCAACCTCTTCCTGCACAAGCACTTCAAACACACATATATTGAGCGGCCTCGTGCT
E L E K D V F V K F D V Y I N S P E H E
AGGGTGGGCGGAGGAGTGAGTTCGCAGGGAGCTTCGTCCACGTGCCACACAAGCA
1621-----+-----+-----+-----+-----+-----+-----+-----+-----+1680
TCCCCACCCCGGCTCCGCTCACTCAAGCGTCCCTCGAAGCAGGTGCACGGTGTGTTCTG
G V G P E A S E F A G S F V H V P H K H
CAAGAAGCGGAAGGGAAGGAGATGCCAGGATGAACACAAGGCTTAAGCTCGGGAT
1681-----+-----+-----+-----+-----+-----+-----+-----+-----+1740
GTTCTTCGGCTTCTTCCCTTCCTCTACCGTCTCTACTTGTGTTCCGAATTCGAGCCCTA
K K A K K G K E M A R M N T R L K L G I
AACGGACCTGCTCGAGGACATCGGGCGCTGAGGACGACGAGAGCGTGCTCATCACGCTCGT
1741-----+-----+-----+-----+-----+-----+-----+-----+-----+1800
TTGCCCTGGACGAGCTCCTGTAGCCGCGACTCCTGTCTCTCGCACGAGTAGTCGAGCA
T D L L E D I G A E D D E S V L I T L V

FIGURE 10G

1801-----+-----+-----+-----+-----+-----+-----+1860
GCCCAGGAGCGGCAAGGGAATGGTGAAGGTTGGAGGGCTAAGGATTGATTCTCTCCAAGTG
CGGGTCCTCGCCGTTCCCTTACCACCTTCCAACCTCCCGATTCTTAACATAAAGAGGTTTCAC
P R S G K G M V K V G G L R I D F S K *
ATGAGCATATTGTGAAGAGAGAAAATTGTCATTACCGCCCTATAGAATCGAAAAAATTGCGT
1861-----+-----+-----+-----+-----+-----+1920
TACTCGTATAACACTTCTCTTTTAAACGTAATGGCGGGATATCTTAGCTTTTAAACGCA
* A Y C E E K I C I Y R P I E S K N C V
ATATGTCCCATTTATTGTTTTTTTATTCTTCAAGCGTATTCAAGAATAAGAGTTGCGTGCA
1921-----+-----+-----+-----+-----+-----+1980
TATACAGGGTAATAACAAAAAATAAGAAAGTTCGCATAAGTCTTATTCTCAACGCACGT
Y V P L L F F L F F K R I Q N K S C V H
TGCACGCATGCAGCCATGTTGTTGTAGTCGATATGTGGGGTATGTTTGATCAGGGATAA
1981-----+-----+-----+-----+-----+-----+2040
ACGTGCGTACGTGCGTACAACAACATCAGCTATACACCCCATACAAACCTAGTCCCTATT
A R M Q P C C C S R Y V G Y V W I R D N
TGATGTGAACCTTGAATTAATTATACACTCTGAGAATAAATTAGAGAGTTTATTATGCA
2041-----+-----+-----+-----+-----+-----+2100
ACTACACTTGAAACTTAATTAATAATGTGAGACTCTTATTTAATCTCTCAATAATACGT
D V N F E L I I T L * E * I R E F I M Q

FIGURE 10H

AGTTGCTTGGTGAATAGATATTCAACATTGTTTCCTATACATCTTTTGGAGAAAA
2101-----+-----+-----+-----+-----+-----+2160

TCAACGAACCATTTATCTATAAGTTGTAACAAGGATATGTAGAAAAAACCTTCTTT
V A W C N R Y S T L F P I H L F L E E K

AAAAAAAAAAAAATCGAT

2161-----+-----+-- 2181

TTTTTTTTTTTTTTAGCTA

K K K K K S

FIGURE 11A

[illegible]

FIGURE 11B

```

301-----+-----+-----+-----+-----+-----+-----+-----+-----+360
      GCGCGCGGATCTGTCCAAGTGCTACCCCTGCCACCGCACCTGCCCTCGACAACAAATGCTG
      CGCGCGCCTAGACAGGTTACACGATGGGACGGTGGCGTGGACGGGAGCTGTTGTTTACGAC
      P P D L S K. C Y P A T A P A L D N K C C
361-----+-----+-----+-----+-----+-----+-----+-----+-----+420
      CCCGCCTTACGACCCCGCGAGACGATCTCGGAGTACAGCTTCCCCTGCTACGCCCTCCG
      GCGCGGAATGCTGGGGCCGCTCTGCTAGAGCCCTCATGTGGAAGGACGATGCGGGGAGGC
      P P Y D P G E T I S E Y S F P A T P L R
421-----+-----+-----+-----+-----+-----+-----+-----+-----+480
      GGTGCGCGCGCCCATATCGTGAAGGACGATCAGGAGTATATGGACAAGTACAAGGA
      CCACGCGCGCGCGGGTATAGCACTTCCTGCTAGTCCCTCATATACCTGTTTCATGTTCTT
      V R R P A H I V K D D Q E Y M D K Y K E
481-----+-----+-----+-----+-----+-----+-----+-----+-----+540
      GGCAGTGAGGAGGATGAAGAATCTGCCGGCAGACCACCCTTGGAACCTACTACCAGCAGGC
      CCGTCACTCCTCCTACTTCTTAGACGGCCGCTCTGGTGGAAACCTTGATGATGGTCGTCGG
      A V R R M K N L P A D H P W N Y Y Q Q A
541-----+-----+-----+-----+-----+-----+-----+-----+-----+600
      GAACATCCACTGCCAGTATTGCAACTACGCCCTACCACCAGCAAAATACCGACGACGTGCC
      CTTGTAGGTGACGGTCATAACGTTGATCGGGATGGTGCTGTTTATGGCTGCTGCACGG
      N I H C Q Y C N Y A Y H Q Q N T D D V P
```

FIGURE 11C

```

CATCCAGGTCCTCAGCTGGATCTCTCCATGGCACCGCTACTACCTCCACTTCTA
601-----+-----+-----+-----+-----+-----+-----+660
GTAGGTCAGGTGAAGTCGACCTAGAAGGAGGTACCGTGGCGATGATGGAGGTGAAGAT
    I  Q  V  H  F  S  W  I  F  L  P  W  H  R  Y  Y  L  H  F  Y
CGAAAGGATCCTCGGCAAGCTCATCGACGACACCTTCACCATCCCATCTGGAACGT
661-----+-----+-----+-----+-----+-----+-----+720
GCTTTCCTAGGAGCCGTTTCGAGTAGCTGCTGTGTGGAAGTGTAGGTAAGACCTTGAC
    E  R  I  L  G  K  L  I  D  D  D  T  F  T  I  P  F  W  N  W
GGACACCAAGGACGGGATGACGTTCCCGCCCATCTTCAGGATGCGGCATCCCCGCTGTA
721-----+-----+-----+-----+-----+-----+-----+780
CCTGTGGTTCCTGCCCTACTGCAAGGGCGGTAGAAGTCTACGCCGTAGGGCGGACAT
    D  T  K  D  G  M  T  F  P  A  I  F  Q  D  A  A  S  P  L  Y
CGACCCGAGACGCGACCAACGCCACGTCAAGGACGGCAAGATCCTCGACCTCAAGTACGC
781-----+-----+-----+-----+-----+-----+-----+840
GCTGGGCTCTGGCTGTTGCGGTGCAGTTCCTGCCGTTCTAGGAGCTGGAGTTCATGCCG
    D  P  R  R  D  Q  R  H  V  K  D  G  K  I  L  D  L  K  Y  A
CTACACCGAAACACTGCATCCGACAGCGAGATCATACGGGAGAACCTCTGCTTCATACA
841-----+-----+-----+-----+-----+-----+-----+900
GATGTGGCTTTGTGACGTAGGCTGTCGCTCTAGTATGCCCTCTTGGAGACGAAGTATGT
    Y  T  E  N  T  A  S  D  S  E  I  I  R  E  N  L  C  F  I  Q
```

FIGURE 11D

```
GAAGACGTTCAAGCACAGCCTGTCGCTGGCGGAACTGTTTCATGGGGGATCCCCGTGCGGCGC
901-----+-----+-----+-----+-----+-----+-----+960
CTTCTGCAAGTTCGTGTCGGACAGCGACCGCCTTGACAAGTACCCCTAGGGCACGCGCG
    K T F K H S L S L A E L F M G D P V R A
GGGGAGAGGAGATCCAGGAGGCTAATGGGCAGATGGAAGTCATCCACAATGCGGCGCA
961-----+-----+-----+-----+-----+-----+-----+1020
CCCCCTCTTCCTCTAGGTCCTCCGATTACCCGCTCTACCTTCAGTAGGTGTTACGCCGCGT
    G E K E I Q E A N G Q M E V I H N A A H
CATGTGGTCTGGAGAGCCGGACGGATACAAGGAAAACATGGGGGACTTCTCCACCGCCGC
1021-----+-----+-----+-----+-----+-----+-----+1080
GTACACCCAGCCTCTCGGCCTGCCCTATGTTCCCTTTGTACCCCTGAAGAGGTGGCGGCG
    M W V G E P D G Y K E N M G D F S T A A
CCGCGATTCTGTTTCTCTGCCACCATTCCAATGTCGACCGCATGTGGGACATCTACCG
1081-----+-----+-----+-----+-----+-----+-----+1140
GGCGCTAAGACAAAAGAAGACGGTGGTAAGGTTACAGCTGGCGTACACCCCTGTAGATGCG
    R D S V F F C H S N V D R M W D I Y R
CAACCTCCGGCAACCGCTCGAGTTCGAAGACAACGACTGTTGGACAGCACCTTCCT
1141-----+-----+-----+-----+-----+-----+-----+1200
GTTGGAGGCGCGGTTGGCGCAGCTCAAGCTTCTGTTGCTGACCAACCTGTCTGGAAGGA
    N L R G N R V E F E D N D W L D S T F L
```

FIGURE 11E

[illegible]

FIGURE 11F

```

1501-----+-----+-----+-----+-----+-----+-----+1560
      GGATATTAAAGTGACCAACGAGACAGCTCGCTTCGACGTCTATGTGCGGTTCCCTTA
      CCTATAATTCCACTGGTGGTTGCTCTGTGCGAGCGAAGCTGCAGATACAGCGCCAAGGAAT
          D I K V T T N E T A R F D V Y V A V P Y

1561-----+-----+-----+-----+-----+-----+-----+1620
      CCGTGACCTCGCCGACCCGACTACGGCGAGTTGCGGGCAGCTACGTGAGGCTGGCGCA
      GCCACTGGAGCGGCTGGGCTGATGCCGCTCAAGCGCCCGTCGATGCACTCCGACCGCGT
          G D L A G P D Y G E F A G S Y V R L A H

1621-----+-----+-----+-----+-----+-----+-----+1680
      TAGGATGAAGGAAGCGACGGGACCGAAAGCAGGGCCCCAAGAAGGAAACTCAA
      ATCCTACTTCCCTTCGCTGCCCTGGCTTTTCGTCCCGGGGTCTTCTTCCCTTTGAGTT
          R M K G S D G T E K Q G P K K K G K L K

1681-----+-----+-----+-----+-----+-----+-----+1740
      GCTGGGTATTACGCCGCTGCTCGAGGACATCGATGCTGAGGACGCCGACAAGTTGGTGGT
      CGACCCATAATGCGGCGACGAGCTCCTGTAGCTACGACTCCTGCGGCTGTTCACACCACCA
          L G I T P L L E D I D A E D A D K L V V

1741-----+-----+-----+-----+-----+-----+-----+1800
      CACCCCTGTTCTCCGCACTGGGAGCGTCACCGTGGGGGGAGTTTCCCATCAATCTCCTGCA
      GTGGACCAAGAGGCGTGACCCCTCGCAGTGGCACCCCCCTCAAGGTAGTTAGAGGACGT
          T L V L R T G S V T V G G V S I N L L Q

```


FIGURE 11G

1801 GACAGATTCTACCGCCGCATCTAAATGATGGCCTCGGATCACAGCTTCTCCCGCTTAA
CTGTCTAAGATGGCGGGTAGATTCTACTACCGGAGCCTAGTGTCTGAAGAGGGGCGGAATT
T D S T A A I *
1861 GTTGAGTGATCGATTACTGGTGTCTTCTTCTCCTCCCTGTCGTTCTTGCTATCTTCTT
CAACCTCACTAGCTAATGACCACGACGAAAGAGGGACAGCAAGAACGATAGAAGAA
1921 GATCTGGAACGATCCTTCAATAATTAGGGCATGACAGTAGTCGTCGCCGATCCCATATG
CTAGACCTTGCTAGGAAGTTATTAATCCCGTACTGTCTATCAGCAGCGGGCTAGGGTATAC
1981 TACGTGTTGGTCTCAACAGCTGTACATGTGACGTTATGGTGTGACTATATATTTATTGC
ATGCACAACCAAGAGTTGTCGACATGTACACTGCAATACCACTGATATATAAAATAACG
2041 GGTCATCCTTGTTTCTTTTAAATAAAAAAAAAA
CCAGTAGGAACAAGAAAGAAATTTTTTTTTTTTTTTT 2078

FIGURE 12A

```

AATGTGGATCGGATGTGGACGGTGTGGAAGAAGCTGCACGGCGACAAAGCCGGAGTTCGTC
1-----+-----+-----+-----+-----+-----+-----+60
TTACACCTAGCCTACACCTGCCACACCTTCTTCGACGTGCCGCTGTTCGGCCTCAAGCAG
  N V D R M W T V W K K L H G D K P E F V

GACCAGGAGTGGCTCGAGTCTGAATTACACCTTCTACGACGAGAATGTGCGCCTGCGCAGG
61-----+-----+-----+-----+-----+-----+-----+120
CTGGTCCCTACCCGAGCTCAGACTTAAGTGGAAGATGCTGCTCTTACACGCGGACGCGTCC
  D Q E W L E S E F T F Y D E N V R L R R

ATCAAGGTGCGCGACGTGTTGAACATAGACAAACTCAGGTACCGGTACGAAGACATCGAC
121-----+-----+-----+-----+-----+-----+-----+180
TAGTTCCACGCGCTGCACAACTTGATCTGTTGAGTCCCATGGCCATGCTTCTGTAGCTG
  I K V R D V L N I D K L R Y R Y E D I D

ATGCCATGGCTCGCTGCACGTCCCAAGCCTTCCGTTCAACCCCTAAGATCGCGCGACATA
181-----+-----+-----+-----+-----+-----+-----+240
TACGGTACCGAGCGACGTGCAGGGTTCGGAAGGCAAGTGGGATTCTAGCGCGCGCTGTAT
  M P W L A A R P K P S V H P K I A R D I

TTGAAGAAGCGTAATGGCGAAGCGGTACTGAGAATGCCCGGCGGAACGGATCGTTCACAA
241-----+-----+-----+-----+-----+-----+-----+300
AACTTCTTCGCATTACCGCTTCCGCATGACTCTTACGGGCGCGCTTTCCTAGCAAGTGT
  L K K R N G E G V L R M P G E T D R S Q
```

FIGURE 12B

```
CTCTCCGAAGATGGTAGCTGGACACTGGACAAGAGCATCACCGTGAGGGTTGACAGGCCA
301-----+-----+-----+-----+-----+-----+-----+360
GAGAGGCTTCTACCATCGACCTGTGACCTGTTCTCGTAGTGGCACCTCCCAACTGTCCGGT
L S E D G S W T L D K S I T V R V D R P

AGGATCAACAGGACAGGGCAAGAAAAGAGGAAGAGAGAGATCTTATTGGTCTACGGA
361-----+-----+-----+-----+-----+-----+-----+420
TCCTAGTTGTCCCTGTCCCGTTCTTTTCTCCTTCTCTCCTCTAGAATAACCATGTCCT
R I N R T G Q E K E E E E I L L V Y G

ATCGATACTAAGAGAAGCAGATTTCGTCAAATTCGATGTGTTCATCAACGTCGTCGACGAA
421-----+-----+-----+-----+-----+-----+-----+480
TAGCTATGATTCTCTTCGTCTAAGCAGTTTAAAGCTACACAAGTAGTTGCAGCAGCTGCTT
I D T K R S R F V K F D V F I N V V D E

ACCGTGTGAACCCAAAGTCGAGGGAGTTCGCAGGGACCTTCGTCAATCTCCACCACGTC
481-----+-----+-----+-----+-----+-----+-----+540
TGGCAGCACTTGGGTTTCAGCTCCCTCAAGCGTCCCTGGAAGCAGTTAGAGGTGGTGCAG
T V L N P K S R E F A G T F V N L H H V

TCGAGGACGAAAAGCCATGAGGATGGCGGGGTTCGAAGATGAAAAGCCACCTTAAG
541-----+-----+-----+-----+-----+-----+-----+600
AGCTCCTGCTTTTCGGTACTCCTACCGCCGCAACCAAGCTTCTACTTTTCGGTGAATTC
S R T K S H E D G G V G S K M K S H L K
```

FIGURE 12C

```

CTCGGTATATCGGAACCTTTGGAAGACCTCGAGGCAGACGAAGATGATTGCATCTGGGTG
601-----+-----+-----+-----+-----+-----+-----+660
GAGCCATATAGCCCTTGAAAACCTTCTGGAGCTCCGCTCTGCTTCTACTAACGTAGACCCAC
L G I S E L L E D L E A D E D D C I W V
ACACTGGTGCCAAGAGGGCGCACGGGGTCAACACCACCGTAGACGGCGTCCGGATCGAC
661-----+-----+-----+-----+-----+-----+-----+720
TGTGACCACGGTTCTCCGCCGTGCCCCAGTTGTGTGGCATCTGCCGAGGCCTAGCTG
T L V P R G G T G V N T T V D G V R I D
TACATGAAGTAGTAACCGGCACGCCGCTCCTCCCCATCAGAAAGTGGTATAATAT
721-----+-----+-----+-----+-----+-----+-----+780
ATGTACTTCATCACTTGGCCGTGCGGCGAGGAGGGGGTAGTCTTCACCATATTATA
Y M K *
TTATATTGGATCGAGGCTCGTGGTATCTTTTGATAAGAGTAAGTCCATAAATTTAGAAG
781-----+-----+-----+-----+-----+-----+-----+840
AATATAACCTAGCTCCGAGCACCATAGAAAACCTATTCTCATTTCAAGGTATTTAAATCTTC
AAGAATCATGTTCTTTATTATTATAATTAAATCAATGTGATTGTCCAAAAAATAAAAAA
841-----+-----+-----+-----+-----+-----+-----+900
TTCTTAGTACAAGAAATAAATAATTAGTTACACTAAACAGGTTTTTTTTTTTTTTT

```

FIGURE 13A

```

TGCACGTGTGCGTATTGCGACGGCGCGTATGACCAAATCGGCTTCCCCGATCTCGAGATCC
1-----+-----+-----+-----+-----+-----+-----+-----+60
ACGTGACACGCATAACGCTGCCGCGCATACTGGTTAGCCGAAGGGCTAGAGCTCTAGG
    H C A Y C D G A Y D Q I G F P D L E I Q
AGATCCACAACCTCGTGGCTCTTCTTCCCTTGGCACCGGTTCTACCTCTACTCCAACGAGC
61-----+-----+-----+-----+-----+-----+-----+-----+120
TCTAGGTGTTGAGCACCGAGAAAGAAAGAACCGTGGCCCAAGATGGAGATGAGGTTGCTCG
    I H N S W L F F P W H R F Y L Y S N E R
GCATACTCGGGAACCTTATCGGCGACGACACGTTGCGCGTGCCTTCTGGAACCTGGGACG
121-----+-----+-----+-----+-----+-----+-----+-----+180
CGTATGAGCCCTTTGAATAGCCGCTGCTGTGCAAGCGCGACGGAAGACCTTGACCCCTGC
    I L G K L I G D D T F A L P F W N W D A
CGCCGGGGCATGCAGTTCCTGCTATCTACACGACCCCTTCATCCTCGCTATATGACA
181-----+-----+-----+-----+-----+-----+-----+-----+240
GGGCCCCCGTACGTCAAGGGCAGATAGATGTGCTGGGAAGTAGGAGCGATATACTGT
    P G G M Q F P S I Y T D P S S S L Y D K
AGCTGCGTGATGCGAAGCACCGCCGCGACTTGTATTGACCTCGACTACAATGGCACCG
241-----+-----+-----+-----+-----+-----+-----+-----+300
TCGACGCACTACGCTTCGTGGTCGGCGGCTGAAACTAACTGGAGCTGATGTTACCGTGGC
    L R D A K H Q P P T L I D L D Y N G T D

```

FIGURE 13B

```

ATCCTACCTTCTCCCTGAAGAACAGATTAAACACAACCTCGCCGTCATGTACCGACAGG
301-----+-----+-----+-----+-----+-----+-----+360
TAGGATGGAAGAGGGGACTTCTTGCTAATTGGTGTGGAGCGGCAGTACATGGCTGTCC
P T F S P E E Q I N H N L A V M Y R Q V

TGATATCCAGTGGAAGACACACAGAGCTGTTTATGGGCTCAGCGTACCGCGCCGGTGACC
361-----+-----+-----+-----+-----+-----+-----+420
ACTATAGGTCACCTTCTGTGGTCTCGACAAATACCGAGTCGCGATGGCGCGGCCACTGG
I S S G K T P E L F M G S A Y R A G D Q

AGCCTGACCCCGCGCAGGCTCTGTAGAGCAGAAGCCGCACGGCCCGGTGCATGTGTGGA
421-----+-----+-----+-----+-----+-----+-----+480
TCGGACTGGGCGCGTCCGAGACATCTCGTCTTCGGCGTGCCGGGCCACGTACACACCT
P D P G A G S V E Q K P H G P V H V W T

CAGGTGATCGCAACCAAGCCCAATCGCGAAGACATGGGCACGCTCTACTCGGCGCGGTGGG
481-----+-----+-----+-----+-----+-----+-----+540
GTCCACTAGCGTTGGTCGGGTTAGCGCTTCTGTACCCGTGCGAGATGAGCCGCCGACCC
G D R N Q P N R E D M G T L Y S A A W D

ACCCCGTCTTCTTCGCACACCAACCGCAACATCGACCGCATGTGGTACGTGTGGAGGAACC
541-----+-----+-----+-----+-----+-----+-----+600
TGGGGCAGAAGCGTGTGGTGCCGTTGTAGCTGGCGGTACACCATGCACACCTCCTTGG
P V F F A H H G N I D R M W Y V W R N L

```

FIGURE 13C

```

601-----+-----+-----+-----+-----+-----+-----+-----+660
      TTGGCGCAAGCACCGCAACTTCACCGACCCCGACTGGCTCAACGCGTCCTTCCTGTTCT
      AACCGCCGTTTCGTGGCGTTGAAGTGGCTGGGGCTGACCGAGTTGCGCAGGAAGGACAAAGA
            G G K H R N F T D P D W L N A S F L F Y
661-----+-----+-----+-----+-----+-----+-----+-----+720
      ATGATGAGAAATGCGCAGCTCGTCCGTGTTAAAGTAAAGACTGCTTAGAGGCCGACGCAA
      TACTACTCTTACGCGTCGAGCAGGCACAAATTTTCATTTTCTGACGAAATCTCCGGCTGCGTT
            D E N A Q L V R V K V K D C L E A D A M
721-----+-----+-----+-----+-----+-----+-----+-----+780
      TCGGGTACACATACCAGGATGTAGAGATCCCCGTGGCTCAAAGCAAAGCCGACGCCAAAGA
      ACGCCATGTGTATGGTCCCTACATCTCTAGGGCACCGAGTTTTCGTTTCGGCTGCGGTTTCT
            R Y T Y Q D V E I P W L K A K P T P K S
781-----+-----+-----+-----+-----+-----+-----+-----+840
      GCGCCCTACAGAAGATAAAGAGCAAGGTATCGACGCTGAAGGCAACACCAAGGGGACGA
      CGCGGGATGTCTTCTATTTCTCGTTCCATAGCTGCGACTTCCGTTGTGGTTCCCCCTGCT
            A L Q K I K S K V S T L K A T P R G T T
841-----+-----+-----+-----+-----+-----+-----+-----+900
      CGACTACCACAGCAGAGACTACATTTCCGGTGGTGTGGATAAGCCGGTGAGTGCAACAG
      GCTGATGGTGTCTCTGTATGTAAAGGCCACCAACGACCTATTCGGGCCACTCACGTTGTC
            T T T A E T T F P V V L D K P V S A T V

```

FIGURE 13D

```

901-----+-----+-----+-----+-----+-----+-----+960
      TGGCTAGACCGAAGGCCAGGAGGAGTGGGAAGGAGAGGAAGAGGAGGAGGTGTTGG
      ACCGATCTGGCTTCCGGTCTCCTCAACCTTCTCCTTCTTCTTCTCCTCCTCCACAACC
          A R P K A R R S G K E K E E E E E V L V
961-----+-----+-----+-----+-----+-----+-----+1020
      TGGTGGAGGGAATCGAGTTGGAGAAGGACGTGTTCTGTAAGTTTGATGTGTATATAAACT
      ACCACCTCCCTTAGCTCAACCTCTTCTCTGCACAAGCACTTCAAACCTACACATATATTGA
          V E G I E L E K D V F V K F D V Y I N S
1021-----+-----+-----+-----+-----+-----+-----+1080
      CGCCGGAGCACGAAGGGTGGGGCCGGAGCGGAGTGAGTTCGCAGGGAGCTTCGTCCACG
      GCGGCCTCGTGCTTCCCAACCCCGCCCTCCGCTCACTCAAGCGTCCCTCGAAGCAGGTGC
          P E H E G V G P E A S E F A G S F V H V
1081-----+-----+-----+-----+-----+-----+-----+1140
      TGCCACACAAGCACAAAGGCGGAAGAGGGAAGGAGATGGCCAGGATGAACACAAGGC
      ACGGTGTGTTTCGTTCTTCCGCTTCTTCCCCCTTCTCTACCCGGTCCCTACTTGTGTTCCG
          P H K H K K A K K G K E M A R M N T R L
1141-----+-----+-----+-----+-----+-----+-----+1200
      TTAAGCTCGGGATAACGGACCTGCTCGAGGACATCGGCGCTGAGGACGACGAGACGCGTGC
      AATTCGAGCCCTATTGCCTGGACGAGCTCCTGTAGCCGCGGACTCCTGCTGCTCTCGCACG
          K L G I T D L L E D I G A E D D E S V L
```


FIGURE 13E

```
TCATCAGCTCGTGCCAGGAGCGGCAAGGAATGGTGAAGTTGGAGGGCTAAGGATTG
1201-----+-----+-----+-----+-----+-----+1260
AGTAGTGGAGCACGGGTCCTCGCCGTTCCCTTACCACCTTCCAACCTCCCGATTCCCTAAC
    I T L V P R S G K G M V K V G G L R I D
ATTTCTCCAAGTGATGAGCATAATTGTGAAGAGAAAAATTTGCATTTACCGCCCTATAGAAT
1261-----+-----+-----+-----+-----+-----+1320
TAAAGAGGTTCACTACTCGTATAACACTTCTCTTTTAAACGTAAATGGCGGGATATCTTA
    F S K * A Y C E E K I C I Y R P I E S
CGAAAAATTGCGGTATATGTCCCATTTATTGTTTTTTTTTTTCTTCAAGCGTATTCAGAATA
1321-----+-----+-----+-----+-----+-----+1380
GCTTTTAAACGCATATACAGGGTAATAACAAAAAATAAGAAGTTCGCATAAAGTCTTAT
    K N C V Y V P L L F F L F F K R I Q N K
AGAGTTGCGTGCAATGCACGCATGCAGCCCATGTTGTTGTAGTCGATATGTGGGGTATGTTT
1381-----+-----+-----+-----+-----+-----+1440
TCTCAACGCACGTACGTGCGTACGTGCGTACAACAACATCAGCTATACACCCCATACAAA
    S C V H A R M Q P C C C S R Y V G Y V W
GGATCAGGGATAATGATGTGAACTTTGAATTAAATTATTACACTCTGAGAAATAATTAGAG
1441-----+-----+-----+-----+-----+-----+1500
CCTAGTCCCTATTACTACACTTGAAACTTAATAATAATGTGAGACTCTTATTTAATCTC
    I R D N D V N F E L I I T L * E * I R E
AGTTTATTATGCAAAAAA
1501-----+-----+--- 1522
TCAAATAATACGTTTTTTTTT
    F I M Q K K
```

FIGURE 14A

```

ACAACAAACAGTGCCTGGTTTAGGTGTATTCACTATGCCACCCCTCTCTAAACTAGCTT
1-----+-----+-----+-----+-----+-----+-----+60
TGTGTTTGGTCACGACCAATCCACATAAGTATACCGTGGGAGAGATTGATCGAA
      N K P V P G L G V F T M A T L S K L A S

CCCCAACCAATAACACCTCCACTCTCCCCGGCTCCCTTTCATGCTCCTTCTCTCACC
61-----+-----+-----+-----+-----+-----+-----+120
GGGTTGGTTATTGTGAGGTGAGAGGGCGGAGGAGAAACGTACGAGGAAGAGAGTGG
      P T N N T S T L P A P S F A C S F S H Q

AAAAGCTTCACCACCACCTTCCTCTCTCCCTGTAGGGTCCCAAAACCCCGTCATAAGA
121-----+-----+-----+-----+-----+-----+-----+180
TTTTCGAAGTGGTGAAGGAGAGGGGACATCCCCAGGTTTGGTGGGGCAGTATCT
      K L H H H L P L P C R G P K P P R H K I

TCTCATGCAAATCTAAGGAGCAACAAGAGAAATGCCGACAAGCCTGCGGGCGCATCGACC
181-----+-----+-----+-----+-----+-----+-----+240
AGAGTACGTTTAGATTCCCTCGTTGTTCTCTTACGGCTGTTCCGACGCCCCGGCGTAGCTGG
      S C K S K E Q Q E N A D K P A G R I D R

GCCGCGACCTACTCCTGGGCCCTCGCGGGGCTTTACGGTGCCACCACCTGGGCTCGGCCTCA
241-----+-----+-----+-----+-----+-----+-----+300
CGCGGCTGGATGAGACCCGAGCGCGCCCGAAATGCCACGGTGTGACCCGAGCCGGAGT
      R D L L L G L G L G L Y G A T T G L G L N

```

FIGURE 14B

```

301-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+360
      ACCGTCGAGCGCGCGCCCTATCCTGGCTCCCGACCTCTCAACTTGTGGCGCGCCTG
      TGGCAGCTCGCCGCGCGGGGATAGGACCGAGGGCTGGAGAGTTGAACACCCGCGGAC
      R R A A A A P I L A P D L S T C G P P A

361-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+420
      CCGACCTCCCTGCCTCCGCCCGACCGACAGTTTGCTGCCCGCATAACCAATCCACCATCA
      GGCTGGAGGACGAGCGGGCTGGCTGTCAAACGACGGCGGTATGGTTAGGTGAGT
      D L P A S A R P T V C C P P Y Q S T I I

421-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+480
      TCGTCTTCAAGCTCCCCCGGATCTGCTCCGCTTCGGTCCGGCTGCGGCCACTTGG
      AGCAGAAAGTTCGAGGGGGCGCTAGACGAGGCGAAGCGCAGCCGACGCCGGTGAACC
      V F K L P P R S A P L R V R P A A H L V

481-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+540
      TTGACGCCGACTACCTGGCCAAGTATAAGAAGCGGTTCGAGCTCATGAGGCCCTGCCCGG
      AACTGCGGCTGATGGACCGGTTTCATATTCTTCGCCAGCTCGAGTACTCCCGGACGGCC
      D A D Y L A K Y K K A V E L M R A L P A

541-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+600
      CCGACGACCCGCGAACTTCGTACAGCAAGCGAAAGTGCACTGTGCGTACTGCGACGGCG
      GGCTGCTGGCGCGTTGAAGCATGTCGTTTCGCTTTCACGTGACACGCGATGACGCTGCCGC
      D D P R N F V Q Q A K V H C A Y C D G A
```

FIGURE 14C

```

CGTACGACCAATCGGCTTCCCGATCTCGAGATCCAGATCCACAACCTCGTGCTCTTCT
601-----+-----+-----+-----+-----+-----+660
GCATGCTGTTTAGCCGAAGGGGCTAGAGCTCTAGGTCTAGGTGTGAGCACCGAGAAGA
    Y D Q I G F P D L E I Q I H N S W L F F
TTCCTTGGCACC GTTCTACCTCTACTTCAACGAGCGCATACTCGGGAACCTTATCGGTG
661-----+-----+-----+-----+-----+-----+720
AAGGAACCGTGGCCAAAGATGGAGATGAAGTTGCTCGCGTATGAGCCCTTTGAATAGCCAC
    P W H R F Y L Y F N E R I L G K L I G D
ACGACACGTTGCGGCTGCCCTTCTGGAACCTGGGACGCGCGGGGGCATGCAGTTCCCGT
721-----+-----+-----+-----+-----+-----+780
TGCTGTGCAAGCGGACGGAAGACCTTGACCCCTGCGCGGCCCCCGTACGTCAAGGGCA
    D T F A L P F W N W D A P G G M Q F P S
CTATCTACACAGACCCTTCATCCTCGCTATATGACAAGCTGCGTGATGCCGAAGCACCAGC
781-----+-----+-----+-----+-----+-----+840
GATAGATGTGCTGGGAAGTAGGAGCGGATATACTGTTGACGCGCACTACGCTTCGTGGTGG
    I Y T D P S S S L Y D K L R D A K H Q P
CGCCGACTTTGATTGACCTCGACTACAATGGCACA
841-----+-----+-----+-----+-----+-----+875
GCGGCTGAAACTAACTGGAGCTGATGTTACCGTGT
    P T L I D L D Y N G T

```

FIGURE 15A

```

1-----+-----+-----+-----+-----+-----+-----+-----+-----+60
GACCACCCATAGATGGCTTCTCTCGCCTTGTCTAGTCTTCCACCTCCACCACAACC
CTGGTGGGTATCTACTACCGAAGAGAGCGGAACAGATCAGAAGGGTGGAGGTGGTGTGG
      M A S L A L S S L P T S T T T
61-----+-----+-----+-----+-----+-----+-----+-----+-----+120
AAAAAACCCCTTATTTCCAAAACATCCTCGCATGTTAAGCCATTCCATCGCTTCAAAGTT
TTTTTTGGGAATAAAAGGTTTGTAGAGCGTACAATTCCGTAAGGTAGCGAAGTTTCAA
      K K P L F S K T S S H V K P F H R F K V
121-----+-----+-----+-----+-----+-----+-----+-----+-----+180
TCATGCAATGCACCCGCTGATAACAATGACAAAACCGTCAATAATTCTGATACCCCAAAG
AGTACGTTACGTGGCGGACTATTGTTACTGTTTGGCAGTTATTAAAGACTATGGGGTTTC
      S C N A P A D N N D K T V N N S D T P K
181-----+-----+-----+-----+-----+-----+-----+-----+-----+240
CTCATACTACCCAAACACCCACTTGAAACGCAGAACGTAGACAGGAGAAACTTGCTTCTG
GAGTATGATGGGTTTGTGGTGAACCTTTGCGTCTTGCATCTGTCTCTTTGAACGAAGAC
      L I L P K T P L E T Q N V D R R N L L L
241-----+-----+-----+-----+-----+-----+-----+-----+-----+300
GGA CTCGGAGGTCTCTACGGCGCTGCCAACTTGACGACCATTCCTCGTCAGCCTTTGGCATT
CCTGAGCCTCCAGAGATGCCCGGACGGTTGAACTGCTGGTAAGGCAGTCGGAAACCGTAA
      G L G G L Y G A A N L T T I P S A F G I

```

FIGURE 15B

```

301-----+-----+-----+-----+-----+-----+-----+360
      C C C A T C G C T G C T C C A G A C A A T A T T C A G A C T G T G T T G C T G C G A C T T C A A A C C T A A G G A A C
      G G G T A G C G A C G A G G T C T G T T A T A A G T C T G A C A C A A C G A C G C T G A A G T T T G G A T T C C T T G
      P I A A P D N I S D C V A A T S N L R N

361-----+-----+-----+-----+-----+-----+-----+420
      A G C A A A G A C G C T A T A A G G G A C T A G C G T G T T G T T C C T C C G G T G C T T T C A A C A A A C A A A C C A
      T C G T T T C T G C G A T A T T C C C C T G A T C G C A C A A C A G G A G G C C A C G A A A G T T G T T G T T T G G T
      S K D A I R G L A C C P P V L S T N K P

421-----+-----+-----+-----+-----+-----+-----+480
      A T G G A T T A C G T C C T T C C T T C A A A C C C T G T G A T T C G T G T T C G A C C A G C T G C A C A G A A A G C C
      T A C C T A A T G C A G G A A G A G T T T G G A C A C T A A G C A C A A G C T G G T C G A C G T G T C T T T C G G
      M D Y V L P S N P V I R V R P A A Q K A

481-----+-----+-----+-----+-----+-----+-----+540
      A C T G C C G A T T A C A C T G C T A A G T A T C A A C A A G C A A T T C A A G C C A T G A A G G A T C T C C C C G A G
      T G A C G G C T A A T G T G A C G A T T C A T A G T T G T T C G T T A A G T T C G G T A C T T C C T A G A G G G G C T C
      T A D Y T A K Y Q Q A I Q A M K D L P E

541-----+-----+-----+-----+-----+-----+-----+600
      G A C C A C C A C A T A G C T G G A A G C A A C A A G G C A A G A T T C A C T G T G C T T A T T G C A A C G G T G G T
      C T G G T G G T A T C G A C C T T C G T T G T T C C G T T C T A A G T G A C A C A G A A T A A C G T T G C C A C C A
      D H P H S W K Q Q Q G K I H C A Y C N G G

```

FIGURE 15C

601-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+660
TACAATCAAGAAACAAAGTGGTTACCCGAATTTACAACCTTCAGATTCACAACCTCATGGCTC
ATGTTAGTTCCTTGTTCACCAATGGGCTTAAATGTTGAAGTCTAAGTGTGAGTACCGAG
Y N Q E Q S G Y P N L Q L Q I H N S W L
TTCTTTTCCTTTCACCGGTGGTACCTCTATTTCTACGAGAAGATATTGGGGAAGTTGATT
661-----+-----+-----+-----+-----+-----+-----+-----+-----+720
AAGAAAGGAAAGGTGGCCACCATGGAGATAAAGATGCTCTCTATAACCCCTTCAACTAA
F F P F H R W Y L Y F Y E K I L G K L I
AATGATCCAACCTTCGCTCTACCTTACTGGAAGTGGGATAACCCCTACTGGAATGGTTATT
721-----+-----+-----+-----+-----+-----+-----+-----+-----+780
TTACTAGGTTGAAAGCGAGATGGAATGACCTTGACCCCTATTGGGATGACCTTACCAATAA
N D P T F A L P Y W N W D N P T G M V I
CCTGCCATGTTCGAACAGAACAGCAAACTAACTCTCTGTTTGACCCCTTTAAGGGATGCG
781-----+-----+-----+-----+-----+-----+-----+-----+-----+840
GGACGGTACAAGCTTGTCTTGTCTGTTTGAATTGAGAGACAAACTGGGAAATTCCTTACGC
P A M F E Q N S K T N S L F D P L R D A
AAACACCTCCACCTTCTATCTTTGATGTTGAATATGCTGGTGCAGACACTGGTGCCACT
841-----+-----+-----+-----+-----+-----+-----+-----+-----+900
TTTGTGGAGGTTGAAGATAGAAACTACAACCTTATACGACCACCGTCTGTGACCACGGTGA
K H L P P S I F D V E Y A G A D T G A T

FIGURE 15D

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TGTATAGACCAGATAGCCATTAACTGTCTTCAATGTACAGACAGATGGTCACCAACTCC
901-----+-----+-----+-----+-----+-----+-----+960
ACATATCTGGTCTATCGGTAATTAGACAGAAGTTACATGTCTGTCTACCAGTGGTTGAGG
C I D Q I A I N L S S M Y R Q M V T N S

ACTGATACAAAACGATTCTTCGGTGGCGAATTGTAGCTGGAAATGACCCTCTTGGGAGC
961-----+-----+-----+-----+-----+-----+-----+1020
TGA CTATGTTTGTAAAGAGCCACCGCTTAAACATCGACCTTTACTGGGAGAACGCTCG
T D T K R F F G G E F V A G N D P L A S

GAGTTCAACGTAGCTGGGACCGTAGAAGCTGGGGTTCACACTGCGGCTCACCGCTGGGTG
1021-----+-----+-----+-----+-----+-----+-----+1080
CTCAAGTTGCATCGACCCCTGGCATCTTCGACCCCAAGTGTGACGCCGAGTGGCGACCCAC
E F N V A G T V E A G V H T A A H R W V

GGTAATTCTAGGATGGCCACACAGCGAAGACATGGGGAACCTTCTACTCCGCAGGATATGAT
1081-----+-----+-----+-----+-----+-----+-----+1140
CCATTAAGATCCTACCGGTTGTCGCTTCTGTACCCCTTGAAGATGAGGCGTCCTATACTA
G N S R M A N S E D M G N F Y S A G Y D

CCTCTCTTTTACGTCCACCATGCGAATGTCGACAGGATGTGGCAAATCTGGAAAGATATT
1141-----+-----+-----+-----+-----+-----+-----+1200
GGAGAGAAAATGCAGGTGGTACGCTTACAGCTGTCCTACACCCGTTTAGACCCTTTCTATAA
P L F Y V H H A N V D R M W Q I W K D I
```


FIGURE 15E

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1201-----+-----+-----+-----+-----+-----+-----+1260
      GACAAGAGACACACAAAGGATCCGACCTCTGGCGACTGGCTAAATGCATCATACGTGTTT
      CTGTTCTTCTGTGTGTTCCTAGGCTGGAGACCGCTGACCGATTACGTTAGTATGCACAAA
      D K K T H K D P T S G D W L N A S Y V F

1261-----+-----+-----+-----+-----+-----+-----+1320
      TAGGATGAGAAATGAAAATCTTGTACGTGTCTACAACCGAGACTGTGTAGACATTAAATCGG
      ATGCTACTCTTACTTTTAGAACATGCACAGATGTTGGCTCTGACACATCTGTAATTAGCC
      Y D E N E N L V R V Y N R D C V D I N R

1321-----+-----+-----+-----+-----+-----+-----+1380
      ATGGGATATGACTACGAAAGGTCAGCAATCCCATGGATCCGTAGTCGGCCGACTGCACAT
      TACCCTATACTGATGCTTTCCAGTCGTTAGGGTACCTAGGCATCAGCCGGCTGACGTGTA
      M G Y D Y E R S A I P W I R S R P T A H

1381-----+-----+-----+-----+-----+-----+-----+1440
      GCGAAGGGGCGAACGTTGCTGCTAAGTCTGCTGGAATCGTGCAGAAGGTGGAGGATATC
      CGCTTCCCCCGCTTGCAACGACGATTTCAGACGACCTTAGCACGTCTTCCACCTCCTATAG
      A K G A N V A A K S A G I V Q K V E D I

1441-----+-----+-----+-----+-----+-----+-----+1500
      GTATTCGCGTGAAGTTAAACAAGATAGTGAAGGTTCTAGTGAAGAGCCAGCTACAAAC
      CATAAGGGCGACTTCAATTTGTTCTATCACTTCCAAGATCACTTCTCCGGTCGATGTTG
      V F P L K L N K I V K V L V K R P A T N
```

FIGURE 15F

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AGGACCAAGGAGGAAAGGAGAAAGCAAATGAGCTGTTGTTTCGTGAATGGAATCACGTTT
1501-----+-----+-----+-----+-----+-----+-----+1560
TCCTGGTTCCCTCCCTTTCCCTCTTTTCGTTTACTCGACAACAAGCACTTACCTTAGTGCAA
R T K E G K E K A N E L L F V N G I T F

GATGCTGAGCGGTTTCTAAAGATTGACGTGTTTGTCAACGACGTCGACGATGGAATTTCAG
1561-----+-----+-----+-----+-----+-----+-----+1620
CTACGACTCGCCAAAGATTTCCTAACTGCACAAACAGTTGCTGCAGCTGCTACCTTAAGTC
D A E R F L K I D V F V N D V D D G I Q

ACCACCGCTGCTGATAGTGAGTTTGCTGGTAGTTTCGCACAGTTGCCACATAACCATGGC
1621-----+-----+-----+-----+-----+-----+-----+1680
TGGTGGCGACGACTATCACTCAAACGACCATCAAAGCGTGTCAACGGTGATTGGTACCG
T T A A D S E F A G S F A Q L P H N H G

GACAAGATGTTTATGAGGAGTGGGGCAGCGTTCGGGATCACGGAGCTCTTGGAAGACATT
1681-----+-----+-----+-----+-----+-----+-----+1740
CTGTTCTACAAATACTCCTCACCCCGTCGCAAGCCCTAGTGCCTCGAGAACCTTCTGTAA
D K M F M R S G A A F G I T E L L E D I

GAAGCTGAAGGTGATGACTCTGTTGTTGTGACATTGGTGCCGAGAACAGGGTGTGATGAA
1741-----+-----+-----+-----+-----+-----+-----+1800
CTTCGACTTCCACTACTGAGACACAACACTGTAAACCGGCTCTTGTCGCCACACTACTT
E A E G D D S V V V T L V P R T G C D E

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FIGURE 15G

GTAACATATTGGCGAGATCAAGATTGCTGGTTCCCATTTGTTAAAGTCTATTGAAGTAA
+-----+-----+-----+-----+-----+-----+
1801

CATTGATAACCGCTCTAGTTCTAAGTCGACCAAGGTAAACAATTTAGATAACTTCATT
V T I G E I K I Q L V P I V *
+-----+-----+-----+-----+-----+-----+
1861

TGCATTTTCAATTGTCTATTAGTAGTGATGCGTGGGTACGTAAATCTGTTGCTGCTGGTTATC
+-----+-----+-----+-----+-----+-----+
1921

ACGTAAAAGTTAACAGTAATCATACGTACCCCATGCATTTAGACAAAGCGACAGACCAATAG
GAGGATTTTTTGATGTTCTCGTAACCAAATAATAAGGATTGTCTATTCCTATGTTTGGAAATCG
+-----+-----+-----+-----+-----+-----+
1981

CTCCTAAAAACTACAAGAGCATTTGGTTTATTATTCTTAACAGTAAGGTACAAAACCTTAGC
TGTAACCGCAGGCATGCATATGTTTGATTTGTTATTTTACTTGAAGCACCTTCTGTTTTAG
+-----+-----+-----+-----+-----+-----+
2041

ACATTGGCGTCCGTACGTATACAAACTAACAAATAAAAAATGAACTTCGTGAAGACAAAAATC
TAAAAAAAAAAAAAAAAA
+-----+-----+-----+-----+-----+-----+
2041

ATTTTTTTTTTTTTTTT